CLAIM AMENDMENTS

1. (Previously Amended) A method of detecting spinocerebellar ataxia type 10 in a sample containing DNA from an individual to be tested comprising the step of measuring the presence or absence of DNA expansion at a spinocerebellar ataxia type 10 gene locus.

2. (Original) The method of claim 1, wherein the expansion is measured by the steps of:

extracting the DNA from a sample to be tested;

amplifying the extracted DNA; and

identifying the presence or absence of a DNA expansion in the amplified extension products.

3. (Original) The method of claim 1, wherein the sample to be tested is selected from the group consisting of blood, semen, saliva, sweat, urine, nipple aspirates, vaginal swabs, tissue, or a combination thereof.

4. (Amended Herein) The method of claim 1, wherein the [amplification] amplifying step is by PCR.

5. (Previously Amended and Amended Herein) The method of claim [1] 4, wherein [the] primers for the PCR are of the sequence from the group consisting of SEQ ID NO: 3 and SEQ ID NO: 4.

6. (Original) The method of claim 1, wherein the DNA expansion is measured by Southern blotting analysis of restriction enzyme digests with a probe to the SCA10 locus.

7. (Amended Herein) The method of claim 6, wherein the restriction [endonuclease]

enzyme is selected from the group consisting of EcoRI, EcoRV, HindIII and BglI.

8. (Previously Amended) The method of claim 6, wherein the probe is created by the use of primers of the sequence from the group consisting of SEQ ID NO: 6 and SEQ ID NO: 7.

9. (Original) The method of claim 1, where the DNA expansion is determined by pulsed field gel electrophoresis.

10. (Original) The method of claim 1, where the DNA expansion is determined by fluorescence in situ hybridization.

11. (Original) The method of claim 1, where the DNA expansion is comprised of a pentanucleotide repeat.

12. (Original) The method of claim 1, where the pentanucleotide repeat is ATTCT.

13. (Original) The method of claim 12, wherein the pentanucleotide repeat is repeated between 10 and 29 times for unaffected individuals and greater than 800 times for individuals affected with spinocerebellar ataxia type 10, with individuals having pentanucleotide repeats in between the normal and expanded range requiring additional study for a diagnosis of spinocerebellar ataxia type 10.

14. (Previously Amended and Amended Herein) A method of detecting pentanucleotide repeats in *SCA10* comprising the steps of:

isolating DNA from an individual to be tested; and

performing PCR analysis using the primers of the sequence from the group consisting of SEQ ID NO: 3 and SEQ ID NO: 4, wherein said PCR analysis detects said pentanucleotide repeats.

15. (Original) The method of claim 14, wherein the pentanucleotide repeat is ATTCT.

16. (Previously Amended and Amended Herein) A method of diagnosing spinocerebellar ataxia type 10 comprising the steps of:

isolating DNA from an individual to be tested;

performing PCR analysis using the primers of the sequence from the group consisting of SEQ ID NO: 3 and SEQ ID NO: 4;

assessing the number of ATTCT repeats based on comparison to DNA from an unaffected individual; and

determining whether the number of ATTCT repeats is expanded in comparison to that of unaffected individuals, wherein when said ATTCT repeats are expanded, said spinocerebellar ataxia type 10 is diagnosed.

17. (Previously Amended and Amended Herein) A method of diagnosing spinocerebellar ataxia type 10 comprising the steps of:

isolating DNA from an individual to be tested;

performing PCR analysis using the primers of the sequence from the group consisting of SEQ ID NO: 10 and SEQ ID NO: 11; and

assessing whether the number of ATTCT repeats is expanded in comparison to that of unaffected individuals, wherein when said ATTCT repeats are expanded, said spinocerebellar ataxia type 10 is diagnosed.

18.-28. (Cancel)